

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: de Boer, Piet A.J.
Hale, Cynthia A.

(ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING
ANTIMICROBIALS

(iii) NUMBER OF SEQUENCES: 25

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 32,837
(C) REFERENCE/DOCKET NUMBER: CASE-02249

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAATACCAAG GATGAAGTAA AGAATTAGTA ATACAATTGC GCGCGGCAGA TACCAGGCAA	60
ATTTTTGCCA TTTCGCGTTTC ATGATTCGCG GCACATCTTT CATGATACCG AAAATCCGG	120
TATCTGGCGG TGTAGCGCCA GTCAATCGTG CTTCCAGTTG TTCAGCCAAT AAACCGTTAA	180
ACGGAGCGGC AATCCAGTTA GCAATCGTGG AGAAGAAATA GCCAAACACT AACAGCACAG	240
AGATGACACG CAGAGGCCAC AACAGATAAC TCAGGCCATTG TAGCCAGTCC GGAACGTAAC	300

TCATGAGAGT CGGGATCCAG ACATCGAGCT GTGTAAAGAG CCACCAGAAT GCGCCCCCA	360
TCAACAAAAT ATTGACCAGC AGCGGTAAAA TAACGAAACG CCGAATCCCA GGTTGCGAGA	420
CGAGCTTCCA GCCTTGCAGA AAATAGTAAA AACCGCTGCG TGGGGCAGAT GTGAATGATG	480
AAACCATAAT CAGGATGAGC TCCTTTGAC CAATCCCAGG AAAATTCTGC GTATTTACC	540
GGGTAATTGC GCAATGGACA GTTAGGATAT GTTCGAAAAA ACAGCAAAA GCACGATTTC	600
ATCTATCTT GTGCTGTGAA AGTTAATAGT GCACTTGCAC TTGAGGTAAT CGGCAAATAC	660
TCTTAGTGAG TAAATGTTG CCGTGGTGGC AAGGTGTTAG AACAAACAGAG AATATAATGA	720
TGCAGGATTT GCGTCTGATA TTAATCATTG TTGGCGCGAT CGCCATAATC GCTTTACTGG	780
TACATGGTTT CTGGACCAGC CGTAAAGAAC GATCTTCTAT GTTCCGCGAT CGGCCATTAA	840
AACGAATGAA GTCAAAACGT GACGACGATT CTTATGACGA GGATGTCGAA GATGATGAGG	900
GCGTTGGTGA GGTCGCGTT CACCGCGTGA ATCATGCCCG GGCTAACGCT CAGGAGCATG	960
AGGCTGCTCG TCCGTCGCCG CAACACCAGT ACCAACCGCC TTATGCGTCT GCGCAGCCGC	1020
GTCAACCGGT CCAGCAGCCG CCTGAAGCGC AGGTACCGCC GCAACATGCT CCGCATCCAG	1080
CGCAGCCGGT GCAGCAGCCT GCCTATCAGC CGCAGCCTGA ACAGCCGTTG CAGCAGCCAG	1140
TTTCGCCACA GGTCGCGCCA GCGCCGCAGC CTGTGCATTC AGCACCGCAA CCGGCACAAC	1200
AGGCTTCCA GCCTGCAGAA CCCGTAGCGG CACCACAGCC TGAGCCTGTA GCGGAACCTG	1260
CTCCAGTTAT GGATAAACCG AAGCGCAAAG AAGCGGTGAT TATCATGAAC GTCGCGCGC	1320
ATCACGGTAG CGAGCTAAC GGTGAAGCTC TTCTTAACAG CATTCAACAA GCGGGCTTCA	1380
TTTTTGGCGA TATGAATATT TACCATCGTC ATCTTAGCCC GGATGGCAGC GGCCCGGCGT	1440
TATTCAGCCT GGCGAATATG GTGAAACCGG GAACCTTGA TCCGTAAATG AAGGATTTC	1500
CTACTCCGGG TGTCACTATC TTTATGCAGG TACCGTCTTA CGGTGACGAG CTGCAGAACT	1560
TCAAGCTGAT GCTGCAATCT GCGCAGCATA TTGCCGATGA AGTGGGCGGT GTCGTGCTTG	1620
ACGATCAGCG CCGTATGATG ACTCCGCAGA AATTGCGCGA GTACCAGGAC ATCATCCGCG	1680
AAGTCAAAGA CGCCAACGCC TGATACACTT AAGGCAAATT AACTCCTCTT CGAACCCCCG	1740
CTTGTGGGG GTTTTAGCA TTGATGGTGC GATATGGAAT CAATCGAACAA ACAACTGACA	1800
GAACTGCGAA CGACGCTTCG CCATCATGAA TATCTTATC ATGTGATGGA TGCGCCGGAA	1860
ATTCCCGACG CTGAATACGA CAGGCTGATG CGCGAACTGC GCGAGCTGGA AACCAAACAT	1920
CCAGAACTGA TTACGCCCTGA TTGCGCTACT CAACGTGTAG GCGCTGCGCC GCTGGCGGCT	1980
TTCAGCCAGA TACGCCATGA AGTACCAATG CTGTCACTGG ATAACGTTTT TGATGAAGAA	2040
AGCTTTCTTG CTTTCAACAA ACGTGTGCAG GACCGTCTGA AAAACAACGA GAAAGTCACC	2100
TGGTGCTGTG AGCTGAAGCT GGATGGTCTT GCCGTCAGTA TTCTGTATGA AAATGGCGTT	2160

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Met Gln Asp Leu Arg Leu Ile Leu Ile Ile Val Gly Ala Ile Ala
1 5 10 15

Ile Ile Ala Leu Leu Val His Gly Phe Trp Thr Ser Arg Lys Glu Arg
20 25 30

Ser Ser Met Phe Arg Asp Arg Pro Leu Lys Arg Met Lys Ser Lys Arg
35 40 45

Asp Asp Asp Ser Tyr Asp Glu Asp Val Glu Asp Asp Glu Gly Val Gly
50 55 60

Glu Val Arg Val His Arg Val Asn His Ala Pro Ala Asn Ala Gln Glu
65 70 75 80

His Glu Ala Ala Arg Pro Ser Pro Gln His Gln Tyr Gln Pro Pro Tyr
85 90 95

Ala Ser Ala Gln Pro Arg Gln Pro Val Gln Gln Pro Pro Glu Ala Gln
100 105 110

Val Pro Pro Gln His Ala Pro His Pro Ala Gln Pro Val Gln Gln Pro
115 120 125

Ala Tyr Gln Pro Gln Pro Glu Gln Pro Leu Gln Gln Pro Val Ser Pro
130 135 140

Gln Val Ala Pro Ala Pro Gln Pro Val His Ser Ala Pro Gln Pro Ala
145 150 155 160

Gln Gln Ala Phe Gln Pro Ala Glu Pro Val Ala Ala Pro Gln Pro Glu
165 170 175

Pro Val Ala Glu Pro Ala Pro Val Met Asp Lys Pro Lys Arg Lys Glu
180 185 190

Ala Val Ile Ile Met Asn Val Ala Ala His His Gly Ser Glu Leu Asn
195 200 205

Gly Glu Ala Leu Leu Asn Ser Ile Gln Gln Ala Gly Phe Ile Phe Gly
210 215 220

Asp Met Asn Ile Tyr His Arg His Leu Ser Pro Asp Gly Ser Gly Pro
225 230 235 240

Ala Leu Phe Ser Leu Ala Asn Met Val Lys Pro Gly Thr Phe Asp Pro
245 250 255

Glu Met Lys Asp Phe Thr Pro Gly Val Thr Ile Phe Met Gln Val
260 265 270

Pro Ser Tyr Gly Asp Glu Leu Gln Asn Phe Lys Leu Met Leu Gln Ser
 275 280 285
 Ala Gln His Ile Ala Asp Glu Val Gly Gly Val Val Leu Asp Asp Gln
 290 295 300
 Arg Arg Met Met Thr Pro Gln Lys Leu Arg Glu Tyr Gln Asp Ile Ile
 305 310 315 320
 Arg Glu Val Lys Asp Ala Asn Ala
 325

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Leu Asn Thr Ile Leu Ile Ile Val Gly Ile Val Ala Leu Val Ala
 1 5 10 15
 Leu Ile Val His Gly Leu Trp Ser Asn Arg Arg Glu Lys Ser Lys Tyr
 20 25 30
 Phe Asp Lys Ala Asn Lys Phe Asp Arg Thr Ser Leu Thr Ser Arg Ser
 35 40 45
 His Thr Gln Glu Glu Met Val Gln Pro Asn Asn Ile Ser Pro Asn Thr
 50 55 60
 Tyr Val Glu Asn Gly His Thr Pro Ile Pro Gln Pro Thr Thr Glu Lys
 65 70 75 80
 Leu Pro Ser Glu Ala Glu Leu Ile Asp Tyr Arg Gln Ser Asp Lys Ser
 85 90 95
 Val Asp Asp Ile Lys Ile Ser Ile Pro Asn Thr Gln Pro Ile Tyr Asp
 100 105 110
 Met Gly Asn His Arg Ser Glu Pro Ile Gln Pro Thr Gln Pro Gln Tyr
 115 120 125
 Asp Met Pro Thr Ala Asn Asn Val Ala Ser Met Thr Leu Glu Gln Leu
 130 135 140
 Glu Ala Gln Ser Gln Asn Val Gly Phe Asn Gly Ile Asn Ser Ser Ser
 145 150 155 160
 Pro Glu Leu Arg Val Gln Leu Ala Glu Leu Ser His Glu Glu His Gln
 165 170 175
 Val Asp Tyr Asn Leu Ser Phe Asn Glu Pro Lys Ala Glu Thr Thr Ala
 180 185 190
 His Pro Lys Gln Thr Thr Gly Tyr Ile Gln Leu Tyr Leu Ile Pro Lys
 195 200 205

Ser Ser Glu Glu Phe Asn Gly Ala Lys Leu Val Gln Ala Leu Glu Asn
210 215 220

Leu Gly Phe Ile Leu Gly Lys Asp Glu Met Tyr His Arg His Leu Asp
225 230 235 240

Leu Ser Val Ala Ser Pro Val Leu Phe Ser Val Ala Asn Leu Glu Gln
245 250 255

Pro Gly Thr Phe Asn Ala Tyr Asn Leu Ala Glu Phe Asn Thr Ile Gly
260 265 270

Ile Val Leu Phe Met Gln Leu Pro Ser Pro Gly Asn Asn Leu Ala Asn
275 280 285

Leu Arg Met Met Met Arg Ala Ala His Thr Leu Ala Glu Asp Leu Gln
290 295 300

Gly Val Ile Leu Thr Glu Glu Gln Glu Ile Phe Asp Ala Asn Ala Glu
305 310 315 320

Gln Ala Tyr Leu Ala Arg Val
325

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ile Leu Ile Ile Val Gly
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /note= "The peptide at this location can be either Arg or Asn."
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 4
 - (D) OTHER INFORMATION: /note= "The peptide at this location can be either Leu or Thr."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Leu Xaa Xaa Ile Leu Ile Ile Val Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Val."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Leu."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Val."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ile Leu Ile Ile Val Gly Xaa Xaa Ala Xaa Xaa Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "The peptide at this location can be either Ala or Leu."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Val."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Leu."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Val."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 14
(D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Leu."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ile Leu Ile Ile Val Gly Xaa Xaa Ala Xaa Xaa Ala Leu Xaa Val His
1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Leu."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Leu Xaa Val His Gly
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Leu."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 7
(D) OTHER INFORMATION: /note= "The peptide at this location can be either Phe or Leu."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Leu Xaa Val His Gly Xaa Trp
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Tyr His Arg His Leu
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= "The peptide at this location can be either Ala or Val."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /note= "The peptide at this location can be either Leu or Val."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Pro Xaa Leu Phe Ser Xaa Ala Asn
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Pro Gly Thr Phe
1

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1

(D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Leu."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Xaa Phe Met Gln
1

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1

(D) OTHER INFORMATION: /note= "The peptide at this location can be either Ile or Leu."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5

(D) OTHER INFORMATION: /note= "The peptide at this location can be either Val or Leu."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Xaa Phe Met Gln Xaa Pro Ser
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACAGAGATCC ATATGATGCA GGATTTGCGT CTG

33

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTAACCAAGC TTAAGTGTAT CAGGCAGTGG

30

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AAGTCTCGAG GGCGTTGGCG TCTTGAC

28

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Glu Asp Pro Pro Ala Glu Phe
1 5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gly His His His His His His His His Ser Ser Gly His
1 5 10 15

Ile Glu Gly Arg His Met Asp Tyr Lys Asp Asp Asp Asp Lys Ala Arg
20 25 30

Arg Ala Ser Val Glu Phe His Met Ala Ser Met Thr Gly Gly Gln Gln
35 40 45

Met Gly Arg Gly Ser
50

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Ala Ser Met Thr Gly Gly Gln Met Gly Arg Gly Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Gly His His His His His His His His Ser Ser Gly His
1 5 10 15

Ile Glu Gly Arg His
20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Asp Tyr Lys Asp Asp Asp Asp Lys Ala Arg Arg Ala Ser Val Glu
1 5 10 15

Phe

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Gly His His His His His His His His Ser Ser Gly His
1 5 10 15

Ile Glu Gly Arg His Met Asp Tyr Lys Asp Asp Asp Asp Lys Ala Arg
20 25 30

Arg Ala Ser Val Glu Phe His Met Ala Ser Met Thr Gly Gly Gln Gln
35 40 45

Met Gly Arg Gly Ser His
50

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGAGGATCCC ATATGTTGA ACCAATGGAA C

31

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTCCGGTCGA CTCTTAATCA GCTTGCTTAC G

31

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